OIPE

RAW SEQUENCE LISTING   DATE: 03/19/2003
PATENT APPLICATION: US/09/627,896B   TIME: 13:12:30

Input Set : A:\08702.0081-01000 seq listing as filed.txt
Output Set: N:\CRF4\03192003\I627896B.raw

```
 3 <110> APPLICANT: CO, MAN SUNG
 4         VASQUEZ, MAXIMILIANO
 5         CARRENO, BEATRIZ
 6         CELNIKER, ABBIE CHERYL
 7         COLLINS, MARY
 8         GOLDMAN, SAMUEL
 9         GRAY, GARY S.
10         KNIGHT, ANDREA
11         O'HARA, DENISE
12         RUP, BONITA
13         VELDMAN, GEERTRUIDA M.
15 <120> TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
16         OF TREATMENT THEREWITH
18 <130> FILE REFERENCE: 08702.0081-01000
20 <140> CURRENT APPLICATION NUMBER: 09/627,896B
```
C--> 21 <141> **CURRENT FILING DATE: 2003-03-11**
```
23 <160> NUMBER OF SEQ ID NOS: 32
25 <170> SOFTWARE: PatentIn Ver. 2.1
```

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

```
714 <210> SEQ ID NO: 22
715 <211> LENGTH: 239
716 <212> TYPE: PRT
717 <213> ORGANISM: Mus sp.
718 <223> OTHER INFORMATION: 3D1 light chain
```
E--> 720 <400> SEQUENCE: 22
```
721 Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Leu Trp Val Ser
722   1               5                  10                  15
724 Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala
725              20                  25                  30
727 Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln Ser
728          35                  40                  45
730 Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln
731      50                  55                  60
733 Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
734  65                  70                  75                  80
736 Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
737                  85                  90                  95
739 Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
740              100                 105                 110
743 Tyr Cys Ser Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln Gly Thr Lys
```

handwritten annotation: >⟨220⟩ ← insert this numeric identifier wherever ⟨221⟩, ⟨222⟩, or ⟨223⟩ is shown

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```
744         115                 120                 125
746 Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
747     130                 135                 140
749 Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
750 145                 150                 155                 160
752 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
753                 165                 170                 175
755 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
756                 180                 185                 190
758 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
759             195                 200                 205
761 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
762     210                 215                 220
764 Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
765 225                 230                 235
1081 <210> SEQ ID NO: 25
1082 <211> LENGTH: 327
1083 <212> TYPE: DNA
1084 <213> ORGANISM: Homo sapiens
1085 <223> OTHER INFORMATION: III2R light chain variable region
```

E--> 1087 <400> SEQUENCE: 25

```
1088 gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc    60
1090 atcacttgcc gggcgagtca gggcattagc aattatttag cctggtatca gcagaaacca   120
1092 gggaaagttc ctaagctcct gatctatgct gcatccactt tgcaatcagg ggtcccatct   180
1094 cggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct   240
1096 gaagatgttg caacttatta ctgtcaaaag tataacagtg cccctccgag tacgttcggc   300
1098 caagggacca aggtggaaat caaacgt                                       327
1101 <210> SEQ ID NO: 26
1102 <211> LENGTH: 339
1103 <212> TYPE: DNA
1104 <213> ORGANISM: Homo sapiens
1105 <223> OTHER INFORMATION: H2F light chain variable region
```

E--> 1107 <400> SEQUENCE: 26

```
1108 gacatccagt tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc    60
1110 atcaactgca agtccagcca gagtgtttta tacagctcca acaacaagaa ttacttaact   120
1112 tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg   180
1114 gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc   240
1116 atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttatagtact   300
1118 cctcgaacgt tcggccaagg gaccaaggtg gaaatcaaa                          339
1121 <210> SEQ ID NO: 27
1122 <211> LENGTH: 95
1123 <212> TYPE: PRT
1124 <213> ORGANISM: Homo sapiens
1125 <223> OTHER INFORMATION: III2R light chain variable region
```

E--> 1127 <400> SEQUENCE: 27

```
1129 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1130 1               5                   10                  15
1132 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
1133             20                  25                  30
```

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PATENT APPLICATION: **US/09/627,896B**   TIME: 13:12:30

Input Set : **A:\08702.0081-01000 seq listing as filed.txt**
Output Set: **N:\CRF4\03192003\I627896B.raw**

```
1135 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
1136          35              40              45
1138 Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
1139      50              55              60
1141 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1142 65              70              75              80
1144 Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Ala Pro
1145              85              90              95
1148 <210> SEQ ID NO: 28
1149 <211> LENGTH: 101
1150 <212> TYPE: PRT
1151 <213> ORGANISM: Homo sapiens
1152 <223> OTHER INFORMATION: H2F light chain variable region
```
E--> 1154 <400> SEQUENCE: 28
```
1156 Asp Ile Gln Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1157 1          5              10              15
1159 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
1160          20              25              30
1162 Ser Asn Asn Lys Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Pro
1163          35              40              45
1165 Pro Lys Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
1166      50              55              60
1168 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
1169 65              70              75              80
1172 Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
1173              85              90              95
1175 Tyr Tyr Ser Thr Pro
1176              100
1179 <210> SEQ ID NO: 29
1180 <211> LENGTH: 368
1181 <212> TYPE: DNA
1182 <213> ORGANISM: Homo sapiens
1183 <223> OTHER INFORMATION: III2R heavy chain variable region
```
E--> 1185 <400> SEQUENCE: 29
```
1186 aggtgcagct ggtgcagtct ggggctgagg tgaagaagcc tgggtcctcg gtaaaggtct    60
1188 cctgcaaggc ttctggaggc accttcagta gttatactat cagctgggtg cgacaggccc   120
1190 ctggacaagg gcttgagtgg atgggaagga tcatgcctat ccttggacta gcaaattacg   180
1192 cacagaagtt ccagggcaga gtcacgatta ccgcggacaa atccacgagc acagcctaca   240
1194 tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgcg agagatcccg   300
1196 attatgtttg ggggagcgac aactggttcg acccctgggg ccagggaacc ctgctcatcg   360
1198 tctcctca                                                           368
1201 <210> SEQ ID NO: 30
1202 <211> LENGTH: 358
1203 <212> TYPE: DNA
1204 <213> ORGANISM: Homo sapiens
1205 <223> OTHER INFORMATION: H2F heavy chain variable region
```
E--> 1207 <400> SEQUENCE: 30
```
1208 gtgcagctgg tggagtctgg gggaggcttg gtcaagcctg gagggtccct gagactctcc    60
1210 tgtgcagcct cggattcacc tttactagga atcctacgag ctgggtacgc caggctccag   120
```

RAW SEQUENCE LISTING   DATE: 03/19/2003
PATENT APPLICATION: US/09/627,896B   TIME: 13:12:31

Input Set : A:\08702.0081-01000 seq listing as filed.txt
Output Set: N:\CRF4\03192003\I627896B.raw

```
1212 ggaaggggct ggagtgggtg gttaatataa tggtagtcgg aattgaacca tactatgcgg   180
1214 actctgtgaa gggccgattc accatctcca gaggcaacgc caagaactca ctgtatctgc   240
1216 aaatgaacag cctgagagcc gaggacacgg ccgtgtatta ctgtgcgaga gggatctgtc   300
1218 ttatgacaga ggctactttg actactgggg ccagggaacc ctggtcaccg tctcctca     358
1221 <210> SEQ ID NO: 31
1222 <211> LENGTH: 97
1223 <212> TYPE: PRT
1224 <213> ORGANISM: Homo sapiens
1225 <223> OTHER INFORMATION: III2R heavy chain variable region
```
E--> 1227 <400> SEQUENCE: 31
```
1229 Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser
1230 1               5                   10                  15
1233 Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr Thr
1234             20                  25                  30
1237 Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1238         35                  40                  45
1241 Arg Ile Met Pro Ile Leu Gly Leu Ala Asn Tyr Ala Gln Lys Phe Gln
1242     50                  55                  60
1245 Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met
1246 65                  70                  75                  80
1249 Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
1250                 85                  90                  95
1253 Arg
1257 <210> SEQ ID NO: 32
1258 <211> LENGTH: 98
1259 <212> TYPE: PRT
1260 <213> ORGANISM: Homo sapiens
1261 <223> OTHER INFORMATION: H2F heavy chain variable region
```
E--> 1263 <400> SEQUENCE: 32
```
1265 Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser
1266 1               5                   10                  15
1269 Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr Tyr
1270             20                  25                  30
1273 Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1274         35                  40                  45
1277 Tyr Ile Ser Ser Arg Gly Ser Glu Thr Ile Tyr Tyr Ala Asp Ser Val
1278     50                  55                  60
1281 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
1282 65                  70                  75                  80
1285 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
1286                 85                  90                  95
1289 Ala Arg
```
E--> 1291 ??
E--> 1293 ??
E--> 1294 (...continued)
E--> 1296 (continued...)

delete

VERIFICATION SUMMARY   DATE: 03/19/2003
PATENT APPLICATION: **US/09/627,896B**   TIME: 13:12:32

Input Set : **A:\08702.0081-01000 seq listing as filed.txt**
Output Set: **N:\CRF4\03192003\I627896B.raw**

L:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:720 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:22
L:881 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 23
L:1087 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:25
L:1107 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:26
L:1127 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:27
L:1154 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:28
L:1185 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:29
L:1207 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:30
L:1227 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:31
L:1263 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:32
L:1291 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:32
L:1291 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1291 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
M:332 Repeated in SeqNo=32
L:1293 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1293 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:1294 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1294 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:1296 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1296 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:1296 M:252 E: No. of Seq. differs, <211> LENGTH:Input:98 Found:100 SEQ:32